

XP-002121206

!!NA_SEQUENCE 1.0

ID AA551623 standard; RNA; EST; 326 BP.

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AC AA551623;

XX

SV AA551623.1

XX

DT 11-SEP-1997 (Rel. 52, Created)

DT 11-SEP-1997 (Rel. 52, Last updated, Version 1)

XX

DE nj57c09.s1 NCI_CGAP_Pr9 Homo sapiens cDNA clone IMAGE:996592.

XX

KW EST.

XX

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;

OC Primates; Catarrhini; Hominidae; Homo.

XX

FN [1]

RP 1-326

FA NCI-CGAP;

RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor

ET Gene Index <http://www.ncbi.nlm.nih.gov/ncicgap>;

RL Unpublished.

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CC Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui,

CC M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CC cDNA Library Preparation: David B. Krizman, Ph.D.

CC cDNA Library Arrayed by: Greg Lennon, Ph.D.

CC DNA Sequencing by: Washington University Genome Sequencing Center

CC Clone distribution: NCI-CGAP clone distribution information can be

CC found through the I.M.A.G.E. Consortium/LLNL at:

CC www-bio.llnl.gov/bbrp/image/image.html

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CC Insert Length: 1374 Std Error: 0.00

CC Seq primer: -40ml3 fwd. ET from Amersham

CC High quality sequence stop: 256.

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FH Key Location/Qualifiers

FH

FT source

FT 1. 326

FT /db_xref="taxon:9606"

FT /db_xref="ESTLIB:925"

FT /note="Organ: prostate; Vector: pAMP10; mRNA made from

FT normal prostatic epithelial cells, cDNA made by oligo-dT

FT priming. Non-directionally cloned. Size-selected on

FT agarose gel, average insert size 600 bp. Library made by

FT D. Krizman, NIH."

FT /sex="male"

FT /organism="Homo sapiens"

FT /clone="IMAGE:996592"

FT /clone_lib="NCI_CGAP_Pr9"

FT /tissue_type="normal prostatic epithelial cells"

PD	11/09/97
P	Coupl. = (2)

FT /lab_host="DH10B"
FT mRNA <1. .>326
XX

SQ Sequence 326 BP; 107 A; 51 C; 44 G; 124 T; 0 other;

Aa551623 Length: 326 November 2, 1999 10:51 Type: N Check: 224 ..

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51  ACTCAGCAAA AGCCATTTAT TATTCAGTGG TATCAAATCT ATCCTATTGT
101 AAAGCACACA GAGACCTTAT CATTCAAACA TTCTTGAAGT GTATGGGTAA

151 ATATTGGAG TTACATTGGA TCTGAATACC AGCAATCAGA ACCATCCTAG
201 GCGATTTCAG ATGCATGATA GATATATTCA ATTAATCAAA AATAAGATGG
251 AAACATTTTA ATAACACTGT CTTTGGCCAT TATTTTATAC AGCATATTTA
301 AAAGTGTTC TTTTATAATT TTTACA
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